Nanoparticles of coal dust and genetic predisposition as risk factors for Chronic Obstructive Pulmonary Disease

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Bronchopulmonary pathology is the leading cause of disability and death among miners in Ukraine. The development of Chronic Obstructive Pulmonary Disease (COPD) is multifactorial and the risk factors of COPD include genetic and environmental ones. Occupational exposure, including organic and inorganic dust, is also a risk factor of COPD [1]. The genetic bases of COPD should also be investigated, similarly to other diseases with complex and multifactorial etiology, by analyzing candidates' genes - genes that are postulated to play an important role in the disease pathogenesis.

Objectives. Functional polymorphism C-1306T (rs243865) in matrix metalloproteinase 2 (*MMP*-2) gene may act as a factor of susceptibility to the development of COPD under the conditions of high coal dust concentration [2].

Methods. The study comprised 72 patients with COPD and 79 healthy miners. The average age of the patients is $53,7 \pm 4,8$ years, the average working age of miners - $22,1 \pm 5,9$ years. The concentration of coal dust in the air of the working area was much higher than normal (from 4.3 to 112.5 times). The diagnosis of COPD was based on spirometry results. Genotyping for the *C-1306T* MMP-2 polymorphism was performed using TaqMan® SNP Assay C_3225943_10 i 7500 Fast Real_time PCR System (Applied Biosystems, Foster City, USA).

Results: There was no significant correlation between patients with MMP2*TT genotype and higher risk of COPD development (p \leq 0,2). However the patients with *T*-allele were at an increased risk of COPD development (p \leq 0,05). This study showed that MMP-9 gene polymorphism C-1306T (rs243865) can be considered as a marker of risk for COPD in Ukrainian miners.

- 1. Global Initiative for Chronic Obstructive Lung Disease. Global Strategy or the Diagnosis, Management and Prevention of Chronic ObstructiveLung Disease. NHLBI/ WHO workshop report. Last update 2011. http://www.goldcopd.com.
- 2. Genetic variation in TIMP1 but not MMPs predict excess FEV1 decline in two general population-based cohorts / van Diemen C.C., Postma D.S., Siedlinski M. [et al.] // Respir Res. 2011. V.12. P. 57–60.